

APPENDIX A

**results of BLAST****BLASTP 2.2.5 [Nov-16-2002]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1048867675-017493-20634

Query=

(256 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

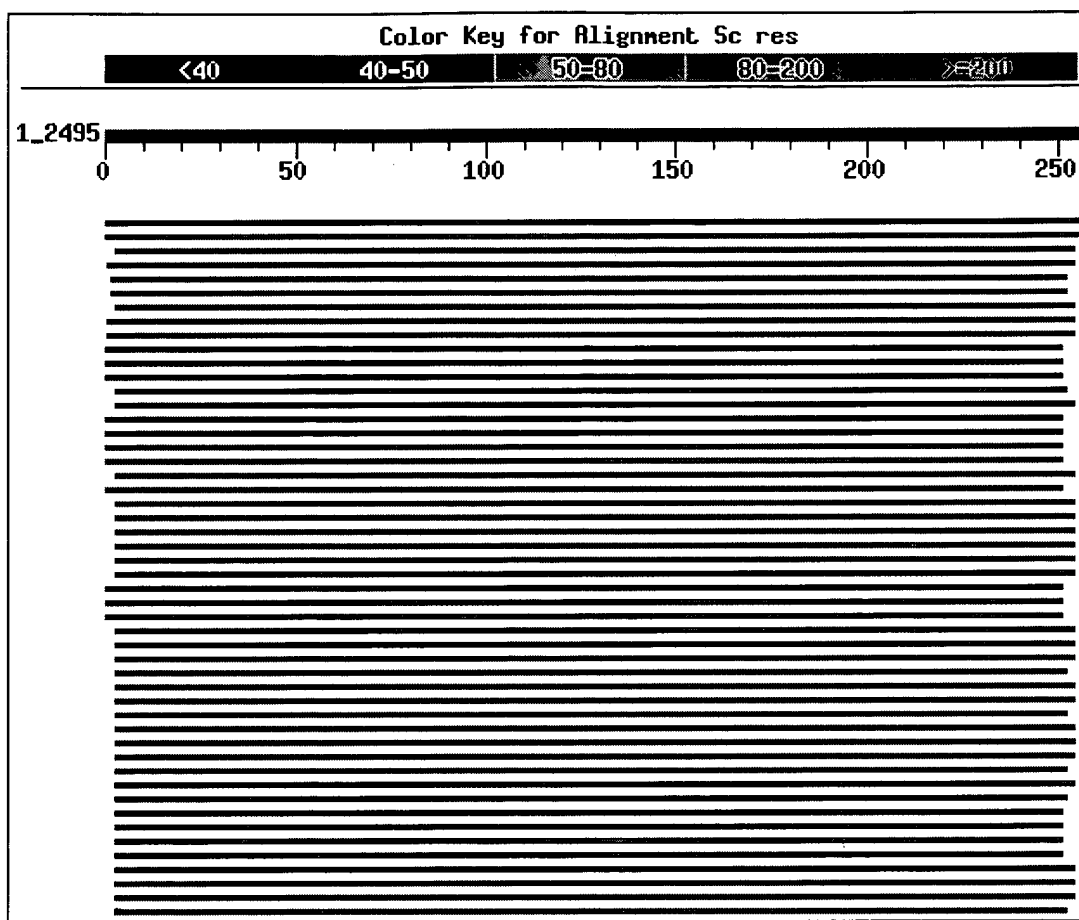
1,384,147 sequences; 445,599,717 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:			Score (bits)	E Value
gi 15924001 ref NP_371535.1 	trans-2-enoyl-ACP reductase [S...		458	e-128
gi 27467630 ref NP_764267.1 	trans-2-enoyl-ACP reductase [S...		424	e-118
gi 21399142 ref NP_655127.1 	adh_short, short chain dehydro...		300	1e-80
gi 15615406 ref NP_243709.1 	enoyl-[acyl-carrier protein] r...		282	3e-75
gi 7531269 sp P54616 FABI_BACSU	Enoyl-[acyl-carrier-protein...		281	6e-75
gi 16078237 ref NP_389054.1 	similar to enoyl- acyl-carrier...		280	1e-74
gi 23097678 ref NP_691144.1 	enoyl-[acyl-carrier protein] r...		248	6e-65
gi 16800038 ref NP_470306.1 	similar to enoyl- acyl-carrier...		244	7e-64
gi 16803010 ref NP_464495.1 	similar to enoyl- acyl-carrier...		244	9e-64
gi 15420715 gb AAK97428.1 AF382392.4	enoyl carrier reductas...		239	3e-62
gi 23128764 gb ZP_00110603.1 	hypothetical protein [Nostoc ...		236	3e-61
gi 13924473 gb AAK49021.1 AF195898.2	enoyl-[acyl-carrier-pr...		234	1e-60
gi 23019970 ref ZP_00059677.1 	hypothetical protein [Clostr...		234	1e-60
gi 23475798 ref ZP_00131074.1 	hypothetical protein [Desulf...		233	3e-60
gi 6686259 sp Q05069 FABI_ANASP	Enoyl-[acyl-carrier-protein...		232	5e-60
gi 17231883 ref NP_488431.1 	enoyl-[acyl-carrier-protein] r...		232	5e-60
gi 23122150 gb ZP_00104285.1 	hypothetical protein [Prochlo...		224	7e-58
gi 23132326 gb ZP_00114111.1 	hypothetical protein [Prochlo...		224	9e-58
gi 23110472 gb ZP_00096626.1 	hypothetical protein [Novosph...		224	1e-57
gi 22299236 ref NP_682483.1 	enoyl-[acyl-carrier-protein] r...		221	1e-56
gi 15964651 ref NP_385004.1 	PUTATIVE ENOYL-ACYL-CARRIER-PR...		219	4e-56
gi 22958522 gb ZP_00006191.1 	hypothetical protein [Rhodoba...		218	5e-56
gi 22963177 gb ZP_00010783.1 	hypothetical protein [Rhodops...		218	6e-56

gi 15888100 ref NP_353781.1	AGR_C_1374p [Agrobacterium tum...	217	1e-55
gi 17987795 ref NP_540429.1	ENOYL-(ACYL-CARRIER-PROTEIN) R...	216	3e-55
gi 13476200 ref NP_107770.1	enoyl-acyl carrier protein red...	216	4e-55
gi 23132906 ref ZP_00114680.1	hypothetical protein [Synech...	214	7e-55
gi 16329628 ref NP_440356.1	enoyl-[acyl-carrier-protein] r...	214	1e-54
gi 6685443 sp P73016 FABI_SYNY3	Enoyl-[acyl-carrier-protein]...	214	1e-54
gi 22966064 gb ZP_00013661.1	hypothetical protein [Rhodosp...	213	2e-54
gi 23055279 gb ZP_00081394.1	hypothetical protein [Geobact...	210	2e-53
gi 27377740 ref NP_769269.1	NADH-enoyl acyl carrier protei...	210	2e-53
gi 23059616 ref ZP_00084568.1	hypothetical protein [Pseudo...	209	4e-53
gi 23015709 gb ZP_00055478.1	hypothetical protein [Magnet...	208	7e-53
gi 22970115 gb ZP_00017264.1	hypothetical protein [Chlorof...	207	8e-53
gi 23103009 gb ZP_00089502.1	hypothetical protein [Azotoba...	207	1e-52
gi 15602047 ref NP_245119.1	FabI [Pasteurella multocida] >...	206	3e-52
gi 13474637 ref NP_106206.1	enoyl-[acyl-carrier-protein] r...	204	9e-52
gi 17988241 ref NP_540875.1	ENOYL-(ACYL-CARRIER-PROTEIN) R...	204	1e-51
gi 15792718 ref NP_282541.1	putative enoyl-[acyl-carrier-p...	203	2e-51
gi 15611251 ref NP_222902.1	ENOYL-ACYL CARRIER PROTEIN RED...	203	2e-51
gi 17545891 ref NP_519293.1	PROBABLE ENOYL-[ACYL-CARRIER-P...	203	2e-51
gi 26247623 ref NP_753663.1	Enoyl-[acyl-carrier-protein] r...	202	4e-51
gi 15801888 ref NP_287908.1	enoyl-[acyl-carrier-protein] r...	202	5e-51
gi 2914323 pdb 1DFG A	Chain A, X-Ray Structure Of Escherich...	202	5e-51
gi 5822339 pdb 1QSG A	Chain A, Crystal Structure Of Enoyl R...	202	5e-51
gi 15672548 ref NP_266722.1	NADH-dependent enoyl-ACP reduc...	201	7e-51
gi 27375882 ref NP_767411.1	NADH-enoyl acyl carrier protei...	201	7e-51
gi 22975990 gb ZP_00021907.1	hypothetical protein [Ralston...	201	7e-51
gi 22982236 ref ZP_00027522.1	hypothetical protein [Burkho...	201	7e-51
gi 6688578 emb CAB65183.1	enoyl reductase [Legionella pneu...	201	8e-51
gi 23469163 ref ZP_00124498.1	hypothetical protein [Pseudo...	200	2e-50
gi 15892417 ref NP_360131.1	putative enoyl-[acyl carrier p...	200	2e-50
gi 22962420 gb ZP_00010026.1	hypothetical protein [Rhodops...	199	2e-50
gi 15604232 ref NP_220748.1	PUTATIVE ENOYL-[ACYL-CARRIER-P...	199	2e-50
gi 28261966 gb EAA25470.1	putative enoyl-[acyl carrier pro...	199	4e-50
gi 28378371 ref NP_785263.1	enoyl-[acyl-carrier protein] r...	198	6e-50
gi 28870876 ref NP_793495.1	enoyl-(acyl-carrier-protein) r...	198	7e-50
gi 16760180 ref NP_455797.1	enoyl-[acyl-carrier-protein] r...	198	8e-50
gi 16765044 ref NP_460659.1	enoyl-[acyl-carrier-protein] r...	197	1e-49
gi 15676251 ref NP_273385.1	enoyl-(acyl-carrier-protein) r...	196	3e-49
gi 23467752 gb ZP_00123331.1	hypothetical protein [Haemoph...	196	3e-49
gi 22955997 gb ZP_00003798.1	hypothetical protein [Nitroso...	195	5e-49
gi 15795023 ref NP_284845.1	enoyl-ACP reductase [Neisseria...	195	5e-49
gi 23000544 gb ZP_00044472.1	hypothetical protein [Magnet...	195	5e-49
gi 16273618 ref NP_439876.1	enoyl-(acyl-carrier-protein) r...	194	1e-48
gi 16127947 ref NP_422511.1	enoyl-(acyl-carrier-protein) r...	194	1e-48
gi 1169593 sp P44432 FABI_HAEIN	Enoyl-[acyl-carrier-protein]...	194	1e-48
gi 15644824 ref NP_206994.1	enoyl-(acyl-carrier-protein) r...	192	4e-48
gi 23015759 gb ZP_00055527.1	hypothetical protein [Magnet...	191	1e-47
gi 15597003 ref NP_250497.1	NADH-dependent enoyl-ACP reduc...	189	3e-47
gi 15963999 ref NP_384352.1	PUTATIVE ENOYL-ACYL-CARRIER-PR...	186	3e-46
gi 23103934 gb ZP_00090406.1	hypothetical protein [Azotoba...	184	1e-45
gi 27378570 ref NP_770099.1	NADH-enoyl acyl carrier protei...	183	2e-45
gi 22961734 gb ZP_00009340.1	hypothetical protein [Rhodops...	182	3e-45
gi 7531116 sp O67505 FABI_AQUAE	Enoyl-[acyl-carrier-protein]...	182	6e-45
gi 15606690 ref NP_214070.1	enoyl-[acyl-carrier-protein] r...	182	6e-45
gi 15806965 ref NP_295690.1	enoyl-acyl carrier protein red...	181	1e-44
gi 24324009 ref NP_715373.1	Enoyl-[acyl-carrier-protein] r...	179	4e-44
gi 22978855 gb ZP_00024594.1	hypothetical protein [Ralston...	178	5e-44
gi 22983971 ref ZP_00029134.1	hypothetical protein [Burkho...	177	1e-43
gi 15887503 ref NP_353184.1	AGR_C_242p [Agrobacterium tume...	173	2e-42

gi 17934067 ref NP_530857.1	enoyl-(acyl-carrier-protein) r...	172	3e-42
gi 22960318 gb ZP_00007959.1	hypothetical protein [Rhodoba...	172	3e-42
gi 22958079 gb ZP_00005759.1	hypothetical protein [Rhodoba...	172	3e-42
gi 22989400 ref ZP_00034455.1	hypothetical protein [Burkho...	172	4e-42
gi 21672535 ref NP_660602.1	enoyl-[acyl-carrier-protein] r...	171	8e-42
gi 22967294 gb ZP_00014888.1	hypothetical protein [Rhodosp...	170	2e-41
gi 27904742 ref NP_777868.1	enoyl-[acyl-carrier-protein] r...	169	3e-41
gi 23010640 gb ZP_00051260.1	hypothetical protein [Magnet...	163	2e-39
gi 15616876 ref NP_240089.1	enoyl-[acyl-carrier-protein] r...	161	1e-38
gi 21220304 ref NP_626083.1	putative enoyl-(acyl-carrier-p...	157	1e-37
gi 23004903 gb ZP_00047997.1	hypothetical protein [Magnet...	145	4e-34
gi 23019834 gb ZP_00059543.1	hypothetical protein [Thermob...	138	8e-32
gi 15618321 ref NP_224606.1	Enoyl-Acyl-Carrier Protein Red...	120	2e-26
gi 14422257 emb CAC41367.1	enoyl-[acyl-carrier protein] re...	117	2e-25
gi 99805 pir S17761	enoyl-[acyl-carrier-protein] reductase...	117	2e-25
gi 7141083 gb AAF37208.1 AF207593_1	enoyl-ACP reductase [Ar...	117	2e-25
gi 15834999 ref NP_296758.1	enoyl-(acyl-carrier protein) r...	117	2e-25
gi 18396215 ref NP_565331.1	enoyl-ACP reductase (enr-A); p...	116	3e-25

Alignments

~ 103

Get selected sequences

Select all

Deselect all

☐ >gi|15924001|ref|NP_371535.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus Mu50]
gi|15926599|ref|NP_374132.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus s N315]
gi|21282621|ref|NP_645709.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus s MW2]
gi|25283453|pir||C89869 trans-2-enoyl-ACP reductase [imported] - Staphylococcus a (strain N315)
gi|6180191|gb|AAF05840.1|AF197058_1 trans-2-enoyl-ACP reductase [Staphylococcus a
gi|13700814|dbj|BAB42110.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus su N315]
gi|14246781|dbj|BAB57173.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus su Mu50]
gi|21204059|dbj|BAB94757.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus su MW2]
Length = 256

Score = 458 bits (1179), Expect = e-128

Identities = 242/256 (94%), Positives = 242/256 (94%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTY QLNQPEA
Sbjct: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLEQLNQPEA 60

Query: 61 HLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
HLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI
Sbjct: 61 HLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120

Query: 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 180
SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP
Sbjct: 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 180

Query: 181 DNIRVNAISAQPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSG 240

DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSG
 Sbjct: 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSG 240

Query: 241 VTGENIHVD SGFHAIK 256
 VTGENIHVD SGFHAIK
 Sbjct: 241 VTGENIHVD SGFHAIK 256

☐ >gi|27467630|ref|NP_764267.1| trans-2-enoyl-ACP reductase [Staphylococcus epider
 gi|27315174|gb|AAO4309.1|AE016746_99 trans-2-enoyl-ACP reductase [Staphylococcus
 Length = 256

Score = 424 bits (1090), Expect = e-118
 Identities = 225/256 (87%), Positives = 233/256 (91%)

Query: 1 MLNLENKTYVIMGIANKR SIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
 MLNLENKTYVIMGIANKR SIAFGVAKVLD+LGAKLVFTY QLNQ E
 Sbjct: 1 MLNLENKTYVIMGIANKR SIAFGVAKVLDRLGAKLVFTYRKERSRKELEKLLEQLNQSEH 60

Query: 61 HLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120
 HLY+IDVQ+DE++INGF QIGKDVG IDGVYHSIAFANMEDLRGRFSETSREGFLLAQ+I
 Sbjct: 61 HLYEIDVQNDEDIINGFSQIGKDVQIDGVYHSIAFANMEDLRGRFSETSREGFLLAQEI 120

Query: 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 180
 SSYSLT+VAHEAKKLMPEGGSIVATTY+GGE AVQNYNVMGVAKASLEANVKYLALDLG
 Sbjct: 121 SSYSLTIVAHEAKKLMPEGGSIVATTYIGGEAAVQNYNVMGVAKASLEANVKYLALDLGE 180

Query: 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSG 240
 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIE RAPLKRNVQ EVGKTAAYLLSDLSSG
 Sbjct: 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEARAPLKRNVQEEVGKTAAYLLSDLSSG 240

Query: 241 VTGENIHVD SGFHAIK 256
 VTGENIHVD GFHAIK
 Sbjct: 241 VTGENIHVDGGFHAIK 256

☐ >gi|21399142|ref|NP_655127.1| adh_short, short chain dehydrogenase [Bacillus ant
 Length = 256

Score = 300 bits (768), Expect = 1e-80
 Identities = 157/252 (62%), Positives = 191/252 (75%)


Query: 4 LENKTYVIMGIANKR SIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L+ KT+V+MG+AN+RSIA+G+A+ L GAKL+FTY L E+ +
 Sbjct: 4 LQGKTFVVMGVANQRSIAWGIARSLHNAGAKLIFTYAGERLERNVRELADTLEGQESLVL 63

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
 DV +DEE+ FE I ++VG I GV H IAFAN +DL+G F +TSR+GFLLAQ+IS++
 Sbjct: 64 PCDVTNDEELTACFETIKQEVGTIIGHVAHCIAFANRDDLKGEFVDTSRDGFLLAQNISAF 123

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SLT VA EAKK+M EGG+I+ TYLGGE V+NYNVMGVAKASLEA+VKYLA DLG I
 Sbjct: 124 SLTAVAREAKKVMTEGGNILTLYLGGERVVKNYNVMGVAKASLEASVKYLANDLGQHG I 183

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVNAISAGPIRTLSAKGVG FN+IL+EIEERAPL+R Q EVG TA +L SDL+ GVTG
 Sbjct: 184 RVNAISAGPIRTLSAKGVGFNSILREIEERAPLRRTTTQEEVGDTAVFLFSDLARGVTG 243

Query: 244 ENIHVDSGFHAI 255
 ENIHVDSG+H +
 Sbjct: 244 ENIHVDSGYHIL 255

 >gi|15615406|ref|NP_243709.1| enoyl-[acyl-carrier protein] reductase [Bacillus l
 gi|25283450|pir||C84005 enoyl-[acyl-carrier protein] reductase BH2843 [imported]
 halodurans (strain C-125)
 gi|10175464|dbj|BAB06562.1| enoyl-[acyl-carrier protein] reductase [Bacillus halo
 Length = 260

Score = 282 bits (722), Expect = 3e-75
 Identities = 149/254 (58%), Positives = 188/254 (74%)


Query: 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAH 61
 L+L ++TYV+MG+ANKRSIA+G+A+ L GA+L+FTY L + +
 Sbjct: 4 LSLVDRTYVVMGVANKRSIAWGIAQSLANAGARLIFTYAGERLEKNVRGLVETLERDDHL 63

Query: 62 LYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDIS 121
 + + DV SDE V F I + VG I G+ H IAFAN E+L G + T+R+GFLLA +IS
 Sbjct: 64 VLECDVTSDEAVEATFASIKEQVGTIHLAHCIAFANKEELEGEYLNTRDGFLLAHNIS 123

Query: 122 SYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPD 181
 +YSLT VA A+ LM EGGIV TYLGGE V+NYNVMGVAKASL+A+VKYLA DLG +
 Sbjct: 124 AYSLTAVAKAARPLMNEGGIVTLTYLGGEKVVRNYNVMGVAKASLDASVKYLANDLGKE 183

Query: 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGV 241
 NIRVNAISAGPIRTL+AKG+GGFN +L+EIEERAPL+R Q EVG TA +L+SDLS G+
 Sbjct: 184 NIRVNAISAGPIRTLAAGGIGGFNDVLR EIEERAPLRRTTTQEEVGDTALFLMSDLRGI 243

Query: 242 TGENIHVDSGFHAI 255
 TGE +HVDSG++ +
 Sbjct: 244 TGEILHVDSGYNIL 257

 >gi|7531269|sp|P54616|FABI_BACSU Enoyl-[acyl-carrier-protein] reductase [NADH]
 enoyl-ACP reductase) (Cold-shock induced protein 15)
 (CSI15) (Vegetative protein 241) (VEG241)
 Length = 258

Score = 281 bits (719), Expect = 6e-75
 Identities = 144/251 (57%), Positives = 183/251 (72%)

Query: 3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHL 62
 +LE + V+MG+ANKRSIA+G+A+ L + GA+L+FTY L++ ++ +
 Sbjct: 4 SLEGRNIVVMGVANKRSIAWGIAARSLHEAGARLIFTYAGERLEKSVHELATGLDRNDSII 63

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122
 DV +D E+ F I + VG I G+ H IAFAN E+L G + T+R+GFLLA +ISS
 Sbjct: 64 LPCDVTND AEIETCFASIKEQVGVHIGIAHCIAFANKEELVGEYLNTRDGFLLAHNISS 123

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YSLT V A+ +M EGGIV TYLGGE + NYNVMGVAKASL+A+VKYLA DLG +N
 YSLTAVVKAARPMTEGGIVTLTYLGGEVMPNYNVMGVAKASLDASVKYLAADLGKEN 183
 3 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242

IRVN+ISAGPIRTLSAKG+ FN+ILK+IEERAPL+R EVG TAA+L SD+S G+T
 Sbjct: 184 IRVNSISAGPIRTLSAKGISDFNSILKDIEERAPLRRTTTTPEEVGDTAAFLFSDMSRGIT 243

Query: 243 GENIHVDSGFH 253
 GEN+HVD SGFH

Sbjct: 244 GENLHVDSGFH 254

☐ >gi|16078237|ref|NP_389054.1| similar to enoyl- acyl-carrier protein reductase [subtilis]
 gi|7431092|pir||G69845 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9
 Bacillus subtilis
 gi|2633526|emb|CAB13029.1| similar to enoyl- acyl-carrier protein reductase [Baci
 subtilis]
 Length = 269

Score = 280 bits (717), Expect = 1e-74
 Identities = 144/251 (57%), Positives = 183/251 (72%)

Query: 3 NLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHL 62
 +LE + V+MG+ANKRSIA+G+A+ L + GA+L+FTY L++ ++ +

Sbjct: 15 SLEGRNIVVMGVANKRSIAWGIARSLHEAGARLIFTYAGERLEKSVHELAGTLDNRDSII 74

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122
 DV +D E+ F I + VG I G+ H IAFAN E+L G + T+R+GFLLA +ISS

Sbjct: 75 LPCDVTNDAEIETCFASIKEQVGVIHGIAHCIAFANKEELVGEYLNTRDGFLLAHNISS 134

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YSLT V A+ +M EGGSIV TYLGGE + NYNVMGVAKASL+A+VKYLA DLG +N

Sbjct: 135 YSLTAVVKAARPMTEGGSIVTLTYLGGEVMPNPNVMGVAKASLDASVKYLAADLGKEN 194

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
 IRVN+ISAGPIRTLSAKG+ FN+ILK+IEERAPL+R EVG TAA+L SD+S G+T

Sbjct: 195 IRVNSISAGPIRTLSAKGISDFNSILKDIEERAPLRRTTTTPEEVGDTAAFLFSDMSRGIT 254

Query: 243 GENIHVDSGFH 253
 GEN+HVD SGFH

Sbjct: 255 GENLHVDSGFH 265

☐ >gi|23097678|ref|NP_691144.1| enoyl-[acyl-carrier protein] reductase [Oceanobaci
 HTE831]
 gi|22775901|dbj|BAC12179.1| enoyl-[acyl-carrier protein] reductase [Oceanobacillu
 Length = 258

Score = 248 bits (633), Expect = 6e-65
 Identities = 135/252 (53%), Positives = 170/252 (67%)

Query: 4 LENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHL 63
 LE K V+MG+AN+RSIA+G+ K L GA L+FT + +

Sbjct: 5 LEGKNIVVMGVANERSIAWGITKSLHNAGANLIFTNRQERSYQKLVKLLDKHEIQAKLIV 64

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 123
 DV DE + F +IG+ VG I GV HS+AFAN ++L+G ++ TSR+GFLLAQ+IS+Y

Sbjct: 65 SCDVADDESIIQAFNEIGKVGVIHGVSVAFANRDELQGEYANTSRDGFLLAQEISAY 124

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183

SL V AK+LM EGG IV TYLG E + YNVMGVAKASLEA+V+YLA D+G I
 Sbjct: 125 SLVAVTKAAKELMTEGGGIVTQTYLGAERVIPGYNVMGVAKASLEASVRYLAEDMGKYGI 184

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVNA+SAGPIRTLSAKGV FN I E+APL+RNVDQ EVG +L+S+++ G+TG

Sbjct: 185 RVNAVSAGPIRTLSAKGVSNFNEKANVIVEKAPLRRNVQDEVGDATLFLVSEMARGITG 244

Query: 244 ENIHVDSGFHAI 255
 E +HVDSGFH I

Sbjct: 245 EVLHVDSGFHII 256

[gi|16800038|ref|NP_470306.1|](#) similar to enoyl- acyl-carrier protein reductase
[gi|25283456|pir||AH1553](#) enoyl- acyl-carrier protein reductase homolog lin0969 [im
 Listeria innocua (strain Clip11262)
[gi|16413428|emb|CAC96200.1|](#) similar to enoyl- acyl-carrier protein reductase [Lis
 Length = 262

Score = 244 bits (624), Expect = 7e-64
 Identities = 135/258 (52%), Positives = 173/258 (67%), Gaps = 4/258 (1%)

Query: 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQ--PE 59
 L+LE KTYV+MG+ANKRSIA+ +A+ L++ GAKLVFTY LN+ +

Sbjct: 3 LSLEGKTYVVMGVANKRSIAWAIARSLNEAGAKLVFTYADDRAKKSITELVPSLNEINQD 62

Query: 60 AHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 + DV S++ + FE I G + G+ H IAFAN + L G + E R+ FL A +

Sbjct: 63 PLILACDVTSEDAITATFETIKDKAGKLSGLAHCIAFANKDYLTGDYLEVDRKSFLQAHE 122

Query: 120 ISSYSLTIVAHEAKKL--MPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALD 177
 IS+YS T VA K L + E S++ TYLGGE V+NYN+MGVAKASL+A+V+YLA+D

Sbjct: 123 ISAYSFTAVARALKHLDMLTEDASLLTLTYLGGERVVENYNIMGVAKASLDASVRYLAM 182

Query: 178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDL 237
 LG +RVNAISAGPIRT+SA+GV GF+ + +EERAPLKR EVG TA YL S+L

Sbjct: 183 LGAIGVRVNAISAGPIRTVSARGVSGFSDSISLVEERAPLKRATQAEVGDATAYYLFSL 242

Query: 238 SSGVTGENIHVDSGFHAI 255
 S GVTGE IHVDSG+H I

Sbjct: 243 SRGVTGEVIHVDSGYHII 260

[gi|16803010|ref|NP_464495.1|](#) similar to enoyl- acyl-carrier protein reductase
 monocytogenes EGD-e]
[gi|25283455|pir||AB1196](#) enoyl- acyl-carrier protein reductase homolog lmo0970 [im
 Listeria monocytogenes (strain EGD-e)
[gi|16410372|emb|CAC99048.1|](#) similar to enoyl- acyl-carrier protein reductase [Lis
 monocytogenes]
 Length = 262

Score = 244 bits (623), Expect = 9e-64
 Identities = 135/258 (52%), Positives = 173/258 (67%), Gaps = 4/258 (1%)

Query: 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAH 61
 L+LE KTYV+MG+ANKRSIA+ +A+ L++ GAKLVFTY L++ +

Sbjct: 3 LSLEGKTYVVMGVANKRSIAWAIARSLNEAGAKLVFTYADDRAKKSITELVPSLSEVNQN 62

Query: 62 --LYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 + DV S+E + FE I G + G+ H IAFAN + L G + E R+ FL A +
 Sbjct: 63 PLILACDVTSEEAITETFTETIKDKAGKLSGLAHCIAFANKDFLTGDYLEVDRKSFLQAHE 122

Query: 120 ISSYSLTIVAHEAKKL--MPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALD 177
 IS+YS T VA K L + E S++ TYLGGE V+NYN+MGVAKASL+A+V+YLA+D
 Sbjct: 123 ISAYSFTAARALKHLEMLTEDASLLTLTYLGGERVVENYNIMGVAKASLDASVRYLAM 182

Query: 178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDL 237
 LG +RVNAISAGPIRT+SA+GV GF+ + +EERAPLKR EVG TA YL S+L
 Sbjct: 183 LGAIGVRVNAISAGPIRTVSARGVSGFSDSISLVEERAPLKRATQAEVGDYAYLFSNL 242

Query: 238 SSGVTGENIHVDSGFHAI 255
 S GVTGE IHVDSG+H I
 Sbjct: 243 SRGVTGEVIHVDSGYHII 260

☐ >gi|15420715|gb|AAK97428.1|AF382392.4 enoyl carrier reductase [Trichodesmium sp.
 gi|23042844|gb|ZP_00074197.1| hypothetical protein [Trichodesmium erythraeum IMS1
 Length = 258

Score = 239 bits (610), Expect = 3e-62
 Identities = 125/253 (49%), Positives = 173/253 (68%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
 MLNL K ++ GIAN RSIA+G+A+ L + GA L TY +
 Sbjct: 1 MLNLTGKNALVTGIANNRSIAWGIAQQLHKAGANLGVTYLPDDKGKFQKKVWELVEPLSP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 LY +VQ D++V F Q+G+ G +D + H +AFA E+L G FS T+REGF A +
 Sbjct: 61 SLYLPCNVQDDQVQKQTFQVGEKWKGLDILIHCLAFAGKEELSGDFSNTTREGFTRALE 120

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
 ISSYSL ++ +AK+LM EGGSII +YLG G V+NYNVMG+AK++LE NV+YLA +LG
 Sbjct: 121 ISSYSLIDLSSKAKELMTEGGSILTSLYLGGRVVRVRYNVMGIAKSALEMNVRYLAAELG 180

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239
 P NIR+NAISAGPIRTL++ VGG ++ +E+ APL+R V Q+E+G TAA+L SDL+S
 Sbjct: 181 PKNIRINAISAGPIRTLASSAVGGILDMIHVEKVAPLRRTVTQIEIGNTA AFLCSDLAS 240

Query: 240 GVTGENIHVDSGF 252
 G+TG+ ++VD+G+
 Sbjct: 241 GITGQVVYVDAGY 253

☐ >gi|23128764|gb|ZP_00110603.1| hypothetical protein [Nostoc punctiforme]
 Length = 258

Score = 236 bits (601), Expect = 3e-61
 Identities = 129/253 (50%), Positives = 170/253 (67%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
 MLNL K ++ GIAN RSIA+G+A+ L + GA L TY +
 Sbjct: 1 MLNLTGKNALVTGIANNRSIAWGIAQQLHKAGANLGVTYLPDERGKMEKKVAELVEPLNP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 L+ +VQ +E++ FE I + G +D + H +AFA+ +DL G FS+TSR GF A +

Sbjct: 61 SLFLPCNVQDEEQIQFTFETIREQWGKLDILIHCLAFASKDDLSGDFSQTSRSGFSTALE 120

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
IS+YSL ++ AK LM EGGIV TYLGG A+ NYNVMGVAKA LE +V+YLA +LG


Sbjct: 121 ISTYSLVQLSGAAKPLMTEGGIVTLTYLGGVRAIPNYNVMGVAKAGLEMSVRYLAAELG 180

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239
P NIRVNAISAGPIRTL++ VGG ++ +EE APL+R V Q+EVG TAA+L SDLSS

Sbjct: 181 PQNIRVNAISAGPIRTLASSAVGGILDMIHHVEEVAPLRRTVTQLEVGNTAAFLCSDLSS 240

Query: 240 GVTGENIHVDSGF 252
G+TG+ ++VD+G+

Sbjct: 241 GITGQVLYVDAGY 253

 >gi|13924473|gb|AAK49021.1|AF195898_2 enoyl-[acyl-carrier-protein] reductase [S] Length = 258

Score = 234 bits (597), Expect = 1e-60
Identities = 129/253 (50%), Positives = 168/253 (66%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
ML+L K ++ GIAN +SIA+G+A+ L GA + TY +

Sbjct: 1 MLDLTGKNALVTGIANNKSIAWGIAQQLHAAGANIGVTYLPDDKGRFEKKVGELVAPLNP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQD 119
L+ +VQ D +V FE + K+ G +D + H +AFAN EDL G FS+TSR+GF A D

Sbjct: 61 SLFLPCNVQDDAQVDQVFESVKKKEWGKLDILIHCLAFANREDLTGDFSQTSRSGFNTALD 120

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
IS+YSLT +A AK +M EGG+IV TYLGG + NYNVMGVAK++LE +V+YLA DLG


Sbjct: 121 ISAYSLTRLARGAKTVMTEGGIAIVTLTYLGGVKVIPNYNVMGVAKSALEMSVRYLAADLG 180

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239
P NIRVNAISAGPIRTL++ VGG ++ +E APL+R V Q EVG AA+L SDLSS

Sbjct: 181 PSNIRVNAISAGPIRTLASSAVGGILDMIHHVEATAPLRRTVTQKEVGNAFLCSDLSS 240

Query: 240 GVTGENIHVDSGF 252
GVTG+ ++VDSG+

Sbjct: 241 GVTGQVLYVDSGY 253

 >gi|23019970|ref|ZP_00059677.1| hypothetical protein [Clostridium thermocellum ?] Length = 252

Score = 234 bits (596), Expect = 1e-60
Identities = 131/250 (52%), Positives = 169/250 (67%), Gaps = 6/250 (2%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L NK ++MG+ NK SIA+G+ K + + GA ++ TY ++

Sbjct: 5 LGNKNILVMGVRNKWSIAWGIVKAVQEEGANVIITYQSEREKEGAEQLGAD-----SIF 58

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQDISSY 123
Q D+ SDEE+ + F I + G + G+ HSIA A EDL+ F TSREGF A +IS+Y

Sbjct: 59 QCDISSDEEINSLFAAIKEKYGVHLGLVHSIAHAKTEDLQNDFIYTSREGFAHAMNISAY 118

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183

SL V+ AK+LM EGGS+ TY+G E + YNVMGVAKA+LEA+V+YLA DLG NI
 Sbjct: 119 SLVAVSRGAKELMTEGGSIIITLYMGSEKVFVKGYNVMGVAKAALEASVRYLAADLGEANI 178

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVGTG 243
 RVNAISAGP++TLAKGV F IL + ++APLKR+ Q ++GKTA YLLSDLSSGVGTG
 Sbjct: 179 RVNAISAGPVKTLAKGVKNFGDILDVPPKAPLKRNTQEDLGKTALYLLSDLSSGVGTG 238

Query: 244 ENIHVDSGFH 253
 E IHVDSG++
 Sbjct: 239 EVIHVDSGYN 248

☐ >gi|23475798|ref|ZP_00131074.1| hypothetical protein [Desulfovibrio desulfuricar]
 Length = 254

Score = 233 bits (593), Expect = 3e-60
 Identities = 123/252 (48%), Positives = 167/252 (66%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L++K +I+G+AN +SIA+G+A+ GA+L F+Y +L +
 Sbjct: 3 LKDKKILILGVANNKSIAYGIAQEFKAQGARLAFSYPGEAIQKRVDPISEELGG--EFTF 60

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
 ++DV D +V + + G++D V HSIAFA EDL GRF +TSREGF LA DIS+Y
 Sbjct: 61 RLDVTDDAQVAAAVRTVEEQWGSVDVVVHSIAFAQREDLHGRFIDTSREGFKLAMDISAY 120

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SL V + LM EGGS++ TY G + + NYNVMGVAKA+LEA+V+YLA D+G I
 Sbjct: 121 SLVCVCKAFEPLMTEGGSVLTMTYYGSQKVITNYNVMGVAKAALEASVRYLAADMGERGI 180

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVGTG 243
 RVNA+SAGPI+TL+A G+ GF TIL IEE APL+RNV +VG+TA +L SDLS VTG
 Sbjct: 181 RVNAVSAGPIKTLAASGISGFKTILNHIEEHAPLRRNVTTQDVGRTAVFLASDLSGAVTG 240

Query: 244 ENIHVDSGFHAI 255
 E + VD+G++ +
 Sbjct: 241 EVLFVDAGYNVM 252

☐ >gi|6686259|sp|Q05069|FABI_ANASP Enoyl-[acyl-carrier-protein] reductase [NADH]
 enoyl-ACP reductase)
 Length = 258

Score = 232 bits (591), Expect = 5e-60
 Identities = 127/253 (50%), Positives = 170/253 (67%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
 MLNL K ++ GIAN RSIA+G+A+ L GA L TY +
 Sbjct: 1 MLNLTGKNALVTGIANNRSIAWGIAQQLHAAGANLGITYLPDERGKFEKKVSELVEPLNP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 L+ +VQ+DE++ + F+ I G +D + H +AFAN +DL G FS+TSR GF A D
 Sbjct: 61 SLFLPCNVQNDEQIQSTFDTIRDKWGRDLILHCLAFANRDDLTDGDFSQTSRAGFATALD 120

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
 IS++SL ++ AK LM EGGS+ +YLG AV NYNVMGVAKA LEA+V+YLA +LG
 Sbjct: 121 ISTFSLVQLSGAAKPLMTEGGSIIITLSYLGAVRPNYNYNVMGVAKAGLEASVRYLASELG 180

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239
NIRVNAISAGPIRTL++ VGG ++ +E+ APL+R V Q+EVG TAA+L SDL+S
Sbjct: 181 SQNIRVNAISAGPIRTLASSAVGGILDMIHHVEQVAPLRRTVTQLEVGNTAAFLASDLAS 240

Query: 240 GVTGENIHVDSGF 252
G+TG+ ++VD+G+
Sbjct: 241 GITGQVLYVDAGY 253

☐ >gi|17231883|ref|NP_488431.1| enoyl-[acyl-carrier-protein] reductase [Nostoc sp.
gi|25283464|pir||AG2354 enoyl-[acyl-carrier-protein] reductase [imported] - Nosto
(strain PCC 7120)
gi|142010|gb|AAD04184.1| unknown [Nostoc sp. PCC 7120]
gi|17133527|dbj|BAB76090.1| enoyl-[acyl-carrier-protein] reductase [Nostoc sp. PC
Length = 264

Score = 232 bits (591), Expect = 5e-60
Identities = 127/253 (50%), Positives = 170/253 (67%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
MLNL K ++ GIAN RSIA+G+A+ L GA L TY +
Sbjct: 7 MLNLTGKNALVTGIANNRSIAWGIAQQQLHAAGANLGITYLPDERGKFEKKVSELVEPLNP 66

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
L+ +VQ+DE++ + F+ I G +D + H +AFAN +DL G FS+TSR GF A D
Sbjct: 67 SLFLPCNVQNDEQIQSTFDTIRDKWGRLDILIHCLAFANRDDLTGDFSQTSRAGFATALD 126

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQYNVVMGVAKASLEANVKYLALDLG 179
IS++SL ++ AK LM EGGS+ +YLG AV NYNVMGVAKA LEA+V+YLA +LG
Sbjct: 127 ISTFSLVQLSGAAKPLMTEGGSIITLSYLGGRVAVPNYNVMGVAKAGLEASVRYLASELG 186

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239
NIRVNAISAGPIRTL++ VGG ++ +E+ APL+R V Q+EVG TAA+L SDL+S
Sbjct: 187 SQNIRVNAISAGPIRTLASSAVGGILDMIHHVEQVAPLRRTVTQLEVGNTAAFLASDLAS 246

Query: 240 GVTGENIHVDSGF 252
G+TG+ ++VD+G+
Sbjct: 247 GITGQVLYVDAGY 259

☐ >gi|23122150|gb|ZP_00104285.1| hypothetical protein [Prochlorococcus marinus suk
CCMP1378]
Length = 260

Score = 224 bits (572), Expect = 7e-58
Identities = 121/255 (47%), Positives = 172/255 (67%), Gaps = 4/255 (1%)

Query: 1 MLNLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQ-- 58
+LNL K ++ GIAN RSIA+G+A+ L + GA+L TY +L QP
Sbjct: 2 LLNLSGKKILVTGIANNRSIAWGIAQQLSKAGAE LGITY-LPDDKGRFESKVRREL TQPLN 60


Query: 59 EAHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQ 118
+ +DVQ+ ++ F+ I + G IDG+ H +AFA ++L G +S T+ EGF A
Sbjct: 61 PSLFLPLDVQNPAQIEEIFKNIKDNWQIDGLVHCLAFAGRDELIGDYSATTSEGFDRAL 120

Query: 119 DISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQYNVVMGVAKASLEANVKYLALDL 178

+IS+YSL + AK L +G +V+ TYLG E A+ NYNVMGVAKA+LEA+V+YL+ +L
 Sbjct: 121 NISAYSLAPLCKAAKPLFSDGAGVVSLTYLGSERAI PNYNVMGVAKAALEASVRYLSAEL 180

Query: 179 GPD-NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDL 237
 GP+ +RVNAISAGPIRTL++ +GG ++ +EE+APL+R V Q EVG TAA+LLSDL
 Sbjct: 181 GPEKQVRVNAISAGPIRTLASSAIGGILDMIHNVEEKAPLRRTVTQTQTEVGNTAAFLSDL 240

Query: 238 SSGVTGENIHVDSGF 252
 SSG++G+ I+VD+G+
 Sbjct: 241 SSGISGQTIYVDAGY 255

 >gi|23132326|gb|ZP_00114111.1| hypothetical protein [Prochlorococcus marinus str.
 Length = 268

Score = 224 bits (571), Expect = 9e-58
 Identities = 119/254 (46%), Positives = 168/254 (66%), Gaps = 2/254 (0%)


Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
 +L+L K ++ GIAN RSIA+G+A+ L GA+L TY E
 Sbjct: 10 LLDLSGKKILVTGIANNRSIAWGIAQQLKAAGAE LGITYLADERGRSE GKVRDLTAPLEP 69

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 L+ ++VQ ++ F I + G +DG+ H +AFA E+L G +S TS EGF A +
 Sbjct: 70 SLFLPLNVQDSNQIEEVFAVIAQQWGLDGLVHCLAFAGKEELVGDYSATSAEGFARALE 129

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
 IS+YSL + H AK L +G +V TYLG + A+ NYNVMGVAKA+LEA+V+YL+ +LG
 Sbjct: 130 ISAYSLAPLCHHAKPLFSDGAGVVTLTYLGADRAIPNYNVMGVAKAALEASVRYLSAELG 189

Query: 180 PD-NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLS 238
 PD +RVNAISAGPIRTL++ +GG ++ +EE+APL+R V Q+EVG TAA+LLSDLS
 Sbjct: 190 PDKQVRVNAISAGPIRTLASSAIGGILEMIHNVEEKAPLRRTVTQIEVGNTAAFLSDLS 249

Query: 239 SGVTGENIHVDSGF 252
 SG++G+ ++VD+G+
 Sbjct: 250 SGISGQTLYVDAGY 263

 >gi|23110472|gb|ZP_00096626.1| hypothetical protein [Novosphingobium aromaticivorans
 Length = 481

Score = 224 bits (571), Expect = 1e-57
 Identities = 117/252 (46%), Positives = 158/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 ++ K +IMG+AN +S+A+G+AK L + GA+L F+Y L L
 Sbjct: 219 MQGKRGLIMGLANDKSLAWGIAKKLHEQGAELAFSYQGEALEKRV RPLAESLGS D--FLI 276

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
 + DV + FE + ID + H+I +++ LRG+F +T+ + FL+ +IS+Y
 Sbjct: 277 ECDVSDMAALDQTFETLKARWPTIDFIVHAIGYSDKNQLRGKFYDTTLDNFLMTMNISAY 336

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SL V A ++MP GGS I+ TY G E V +YNVMGVAKA+LEA+VKYLA D GP I
 Sbjct: 337 SLVAVTKRAAEMMPAGGSILTLYYGAEKVVPHYNVMGVAKAALEASVKYLANDCGPAGI 396

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVNAISAGPI+TL+A G+G F ILK E +PL+RNV +VG Y LSDLSSGVTG
 Sbjct: 397 RVNAISAGPIKTLAASGIGDFRYILKWNELNSPLRRNVTIEDVGGAGLYFLSDLSSGVTG 456

Query: 244 ENIHVDSGFHAI 255
 E HVD+G+H +
 Sbjct: 457 ETHHVDAGYHTV 468

☐ >gi|22299236|ref|NP_682483.1| enoyl-[acyl-carrier-protein] reductase [Thermosynechococcus
 elongatus BP-1]
 gi|22295418|dbj|BAC09245.1| enoyl-[acyl-carrier-protein] reductase [Thermosynechococcus
 elongatus BP-1]
 Length = 259

Score = 221 bits (562), Expect = 1e-56
 Identities = 123/253 (48%), Positives = 161/253 (63%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTY-XXXXXXXXXXXXXXXXXQLNQPE 59
 +L+L K ++ GIAN RSIA+G+A+ + GA+L TY
 Sbjct: 2 LLDLSGKRALVTGIANNRSIAWGIAQQIHAAGAELAVTYLPDERGKLGKQKVEELTAPLVP 61

Query: 60 AHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQD 119
 L +DVQ +++ + F I G +D + H +AFA EDL G FS S EGF LA D
 Sbjct: 62 KLLLPLDVQPPQQIDDVFAAIQSTWGGLDILIHCLAFAQKEDLNGDFSASVLEGFHLALD 121

Query: 120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQYNVVMGVAKASLEANVKYLALDLG 179
 IS+YSL ++ AK LM GGS+ TYLGG V NYNVMG+AKA+LE NV+YLA +LG
 Sbjct: 122 ISAYSLISLSRAAKPLMTHGGSIIITLTYLGGVRVVPNYNVMGIAKAALEMNVRYLAAELG 181

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239
 P NIRVN ISAGPIRTL++ VGG ++ +E APL+R V Q EVG TAA+L SDL+S
 Sbjct: 182 PRNIRVNGISAGPIRTLASSAVGGILDMIHVEATAPLRRTVTQTEVGNTAAFLASDLAS 241

Query: 240 GVTGENIHVDSGF 252
 G+TG+ ++VDSG+
 Sbjct: 242 GITGQILYVDSGY 254

☐ >gi|15964651|ref|NP_385004.1| PUTATIVE ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE NADH [S
 meliloti]
 gi|17366329|sp|P58380|FAI1_RHIME Enoyl-[acyl-carrier-protein] reductase [NADH] 1
 enoyl-ACP reductase 1)
 gi|15073829|emb|CAC45470.1| PUTATIVE ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE NADH [S
 meliloti]
 Length = 272

Score = 219 bits (557), Expect = 4e-56
 Identities = 126/253 (49%), Positives = 164/253 (64%), Gaps = 4/253 (1%)

Query: 4 LENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA-HL 62
 + K VIMG+AN RSIA+G+AK L + GA++ T+ +L A H
 Sbjct: 8 MNGKRGVIMGVANNRSIAWGIAKALAEAGAEIALTWQGDALKKRVEPLAQELGAFMAGHC 67

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQDISS 122
 D+ + + V + E+ G ID V H+IAF++ ++L GR+ +TSR+ F DIS
 Sbjct: 68 DVTDLATIDAVFSALEE---KWGKIDFVVHAIASFSDKDELDTGRYLDTSRDNFARTMDISV 124

Query: 123 YSLTIVAHEAKKLMPEGGSSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YS T VA A ++M +GCSI+ TY G E + +YNVMGVAKA+LEA+V+YLA+DLG
 Sbjct: 125 YSFTAVAAARADRVMDGGSILTLTYYGAEKVMPHYNVMGVAKAALEASVRYLAVDLGNRG 184

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
 IRVNAISAGPI+TL+A G+G F ILK E APLKR V EVG +A YLLSDLSSGVT
 Sbjct: 185 IRVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLKRTVSIEEVGNSALYLLSDLSSGVT 244

Query: 243 GENIHVDSGFHAI 255
 GE HVDSG+H +
 Sbjct: 245 GEVHHVDSGYHTV 257

☐ >gi|22958522|gb|ZP_00006191.1| hypothetical protein [Rhodobacter sphaeroides]
 Length = 274

Score = 218 bits (556), Expect = 5e-56
 Identities = 115/252 (45%), Positives = 158/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L K +IMG+AN +SIA+G+AK GA+L F+Y + E +
 Sbjct: 6 LAGKRGLIMGLANDKSIAWGIACCADQGAELAFSYQGDALKKRVEPLAASIGATE--MV 63

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQDISSY 123
 + DV + + F + + G +D V H+I F++ +LRGR+ +T+ F + DIS Y
 Sbjct: 64 ECDVSDEASLDRFLFAHLKEVWGTLDFVVAIGFSDKSELRGYVDTTTPANFRMTMDISVY 123

Query: 124 SLTIVAHEAKKLMPEGGSSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 S T V A +MP GGS++ TY G E + +YNVMG+AKA+LE +V+Y+A DLG D I
 Sbjct: 124 SFTAVCQRACAMMPAGGSLTLTLTYYGAEKVMPHYNVMGIAKAALETSVQYIAEDLGKDG I 183

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVNAISAGPI+TL+A G+G F I+K E +PL+RNV Q EVGK A YLLSDL SG TG
 Sbjct: 184 RVNAISAGPIKTLAASGIGDFRYIMKWNEINSPLRRNVTQEEVGKAALYLLSDLGSGTTG 243

Query: 244 ENIHVDSGFHAI 255
 E +HVD+G+H +
 Sbjct: 244 EVLHVDAAGYHV 255

☐ >gi|22963177|gb|ZP_00010783.1| hypothetical protein [Rhodopseudomonas palustris]
 Length = 273

Score = 218 bits (556), Expect = 6e-56
 Identities = 124/252 (49%), Positives = 160/252 (63%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 ++ K VI+G+AN RSIA+G+AK GA++ TY +L L
 Sbjct: 8 MQGKRGVILGVANNRSIAWGIACACRAQGAELIALTYQGDALKKRVEPLAAELGG--LVLG 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQDISSY 123
 DV + F+ + + G ID V H+IAFA+ ++L GR+ +TS E F + IS Y
 Sbjct: 66 HCDVTDGATIDAVFDAVKEKWGKIDFVVAIAFADKDELDRYVDTSFENFSKSMILISCY 125

Query: 124 SLTIVAHEAKKLMPEGGSSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SLT +A A+KLM +GCSI+ TY G E + +YNVMGVAKA+LEA+V+YLA DLG NI

Sbjct: 126 SLTAIAQRAEKLMTDGGSIITLTYYGAEKWMPHYNVMGVAKAALEASVRYLAADLGEKNI 185

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSSGVTG 243
RVNAISAGPI+TL+A G+G F ILK E APL+R V EVG +A Y LSDLS GVTG

Sbjct: 186 RVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLRRTVTIEEVGDSALYFLSDLRSGVTG 245

Query: 244 ENIHVDSGFHAI 255
E HVDSG+H +

Sbjct: 246 EVHHVDSGYHVV 257

>gi|15888100|ref|NP_353781.1| AGR_C_1374p [Agrobacterium tumefaciens]
gi|17934667|ref|NP_531457.1| enoyl-(acyl-carrier-protein) reductase [NADH] [Agrobacterium tumefaciens str. C58 (U. Washington)]
gi|25283457|pir||E97451| hypothetical protein AGR_C_1374 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
gi|25283463|pir||AG2669| enoyl-(acyl-carrier-protein) reductase [NADH] fabI [imported] Agrobacterium tumefaciens (strain C58, Dupont)
gi|15155730|gb|AAK86566.1| AGR_C_1374p [Agrobacterium tumefaciens str. C58 (Cereon)]
gi|17739126|gb|AAL41773.1| enoyl-(acyl-carrier-protein) reductase [NADH] [Agrobacterium tumefaciens str. C58 (U. Washington)]
Length = 272

Score = 217 bits (553), Expect = 1e-55

Identities = 124/252 (49%), Positives = 161/252 (63%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
+ K +IMG+AN RSIA+G+AK GA+L T+ +L A

Sbjct: 8 MAGKRGLIMGVANNRSIAWGIACACADAGAEALALTWQGDALKKRVEPLAQELGAFMAG-- 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQDISSY 123
DV E + + F + + G ID V H+IAF++ ++L GR+ +TSR+ F DIS +

Sbjct: 66 HCDVTDLETIDSVFASLEQHWGKIDFVVHAIASFSDKDELDTGRYLDTSRDNFNRTMDISVF 125

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
SL VA A+ +M +GGS+ TY G E + NYNVMGVAKA+LEA+V+YLA+DLG I

Sbjct: 126 SLAAVAKRAEPIMNDDGGSIITLTYYGAEKVMPNYNVMGVAKAALEASVRYLAVDLGNRGI 185

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSSGVTG 243
RVNA+SAGPI+TL+A G+G F ILK E APLKR V EVGK+A YLLSDLS+ VTG

Sbjct: 186 RVNAVSAGPIKTLAASGIGDFRYILKWNEYNAPLKRTVTIEEVGKSALYLLSDLSTAVTG 245

Query: 244 ENIHVDSGFHAI 255
E HVDSG+H I

Sbjct: 246 EIHVDSGYHTI 257

>gi|17987795|ref|NP_540429.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella melitensis (strain 16M)]
gi|23501323|ref|NP_697450.1| enoyl-(acyl-carrier-protein) reductase [Brucella suis (strain 16M)]
gi|25283461|pir||AB3441| enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.1) [imported] - Brucella melitensis (strain 16M)
gi|17983520|gb|AAL52693.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella melitensis (strain 16M)]
gi|23347213|gb|AAN29365.1|AE014352.11 enoyl-(acyl-carrier-protein) reductase [Brucella melitensis (strain 16M)]
Length = 272

Score = 216 bits (550), Expect = 3e-55

Identities = 124/252 (49%), Positives = 157/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L+ K +I+G+AN RSIA+G+AK + GA+L FTY +L A
Sbjct: 8 LQGKRGLILGVANNRSIAWGIAKAAREAGAELAFETYQGDALKKRVEPLAEELGAFVAG-- 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
DV + FE + K G +D + H+I F++ ++L GR+ +TS F IS Y
Sbjct: 66 HCDVADAASIDAVFETLEKKWGKLDLFLVHAIGFSDKDELDTGRYIDTSEANFTNTMLISVY 125

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
SLT V+ A+KLM +GGSI+ TY G E + NYNVMGVAKA+LEA+VKYLA+DLGP NI
Sbjct: 126 SLTAVSRRAEKLMDGGSILTLTYGAEKVMPNYNVMGVAKAALASVKYLAVDLGPDNI 185

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
RVNAISAGPI+TL+A G+G F ILK E APL+R V EVG Y LSDLS VTG
Sbjct: 186 RVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLRRTVTIDEVGDVGLYFLSDLRSRVTG 245

Query: 244 ENIHVDSGFHAI 255
E H DSG+H I
Sbjct: 246 EVHHADSGYHVI 257

☐ >gi|13476200|ref|NP_107770.1| enoyl-acyl carrier protein reductase [Mesorhizobium loti]
gi|14026960|dbj|BAB53556.1| enoyl-acyl carrier protein reductase [Mesorhizobium loti]
Length = 272

Score = 216 bits (549), Expect = 4e-55

Identities = 122/253 (48%), Positives = 161/253 (63%), Gaps = 4/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA-HL 62
+ K +I+G+AN RSIA+G+AK GA++ TY +L A H
Sbjct: 8 MAGKRGLILGIANNRSIAYGIAKACVDHGAELTYQGEAFKKRVEPLAAELGAFVAGHC 67

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122
D S +EV F + K G +D + H+IAF++ ++L GR+ ET+R+ FL DIS
Sbjct: 68 DVTDSASLDEV---FANVAKHWGKLDLFLVHAIAFSDKDELDTGRYVETTRDNFLRTMDISV 124

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
+S T +A A+ LM EGGS++ TY G E + +YNVMGVAKA+LEA+V+YLA+DLG
Sbjct: 125 FSFTTIKRAEALMTEGGSLLTLTYGAEKVMPHYNVMGVAKAALASVRYLAVDLGGKK 184

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
IRVNAISAGPI+TL+A G+G F ILK E +PLK+ V Q EVG + Y LSDLS GVT
Sbjct: 185 IRVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLQTVTQEEVGDSGVYFLSDLRSRVT 244

Query: 243 GENIHVDSGFHAI 255
GE HVDSG+H +
Sbjct: 245 GEVHHVDSGYHVV 257

☐ >gi|23132906|ref|ZP_00114680.1| hypothetical protein [Synechococcus sp. WH 8102]
Length = 260

Score = 214 bits (546), Expect = 7e-55

Identities = 116/254 (45%), Positives = 167/254 (65%), Gaps = 2/254 (0%)

Query: 1 MLNLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEA 60
 +L+L K ++ GIAN RSIA+G+A+ L GA+L TY E
 Sbjct: 2 LLDLTGKKILVTGIANNRSIAWGIAQQLKAAGAEIGITYLPDDKGRFEAKVRELTAPEL 61

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119
 L+ ++VQ +++ F +I G +DG+ H +AFA E+L G +S T+ EGF + D
 Sbjct: 62 SLFLPLNVQDADQMAEVFGEIKAKWGVLDGLVHCLAFAGKEELIGDYSATTAEGFARSLD 121

Query: 120 ISSYSLTIVAHEAKKLMPEGGSI VATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
 IS+YSL + AK L E ++ +YLG E A+ NYNVMGVAKA+LEA+V+YLA +LG
 Sbjct: 122 ISAYSLAPLCAHAKPLFSEKAGVITLSYLGAERAIPNYNVMGVAKAALEASVRYLAAELG 181

Query: 180 PD-NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLS 238
 P+ +RVNAISAGPIRTL++ +GG ++ +EE+APL+R V Q+EVG TAA+LLSDL+
 Sbjct: 182 PEKQVRVNAISAGPIRTLASSAIGGILDMIHNVEEKAPLRRTVTQMEVGGTAAFLSLDLA 241

Query: 239 SGVTGENIHVDSGF 252
 SG++G+ I+VD+G+
 Sbjct: 242 SGISGQTIYVDAGY 255

☐ >gi|16329628|ref|NP_440356.1| enoyl-[acyl-carrier-protein] reductase [Synechocystis
 gi|7427661|pir||S74996 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9
 Synechocystis sp. (strain PCC 6803)
 gi|1652111|dbj|BAA17036.1| enoyl-[acyl-carrier-protein] reductase [Synechocystis
 Length = 278

Score = 214 bits (545), Expect = 1e-54

Identities = 120/254 (47%), Positives = 160/254 (62%), Gaps = 3/254 (1%)

Query: 1 MLNLENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQ-- 58
 ML+L K + GIAN RSIA+G+A+ L Q GA++ +Y +L +P
 Sbjct: 21 MLDLSGKHAFVTGIANNRSIAWGIAQQLHQAGAEIGVSY-LPDEKGRFEKKVRELTEPLH 79

Query: 59 EAHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQ 118
 + DVQ D +V F + + G +D + H +AFA+ L G +++ +E F A
 Sbjct: 80 PTLVLPGDVQDDAQVDALFHSVKEKWGKLDILIHCLAFADKSGLTGNYTDIPKEAFSQAM 139

Query: 119 DISSYSLTIVAHEAKKLMPEGGSI VATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDL 178
 +IS+YSL +A AK LM GGS+ TY GG + NYN+MGVAKA LE V+YLA +L
 Sbjct: 140 EISTYSLGRLARGAKPLMTNGGSIITLTYFGGVKVIPNYNLMGVAKAGLEMTVRYLAAEL 199

Query: 179 GPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLS 238
 GP NIRVN ISAGPIRTL++ VGG ++ +EE APLKR V Q EVG TAA+L SDLS
 Sbjct: 200 GPQNIRVNGISAGPIRTLASSAVGGILDMIHHVEEVAPLKRVTQTQTEVGNTAAFLASDL 259

Query: 239 SGVTGENIHVDSGF 252
 SG+TG+ I+VDSG+
 Sbjct: 260 SGITGQIIYVDSGY 273

☐ >gi|6685443|sp|P73016|FABI_SYNY3 Enoyl-[acyl-carrier-protein] reductase [NADH]
 enoyl-ACP reductase)
 Length = 258

Score = 214 bits (544), Expect = 1e-54

Identities = 120/254 (47%), Positives = 160/254 (62%), Gaps = 3/254 (1%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQP-- 58
 ML+L K + GIAN RSIA+G+A+ L Q GA++ +Y +L +P
 Sbjct: 1 MLDLSGKHAFVTGIANNRSIAWGIAQQLHQAGAEIGVSY-LPDEKGRFEKKVRELTEPLH 59

Query: 59 EAHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQ 118
 + DVQ D +V F + + G +D + H +AFA+ L G +++ +E F A
 Sbjct: 60 PTLVLPGDVQDDAQVDALFHSVKEKWGKLDILIHCLAFADKSGLTGNYTDIPKEAFSQAM 119

Query: 119 DISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDL 178
 +IS+YSL +A AK LM GGS+ TY GG + NYN+MGVAKA LE V+YLA +L
 Sbjct: 120 EISTYSLGRLARGAKPLMTNGGSIITLTYFGGVKVIPNYNLMGVAKAGLEMTVRYLAAEL 179

Query: 179 GPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLS 238
 GP NIRVN ISAGPIRTL++ VGG ++ +EE APLKR V Q EVG TAA+L SDLS
 Sbjct: 180 GPQNIRVNGISAGPIRTLASSAVGGILDMIHHVEEVAPLKRTVTQTEVGNTAAFLASDLS 239

Query: 239 SGVTGENIHVDSGF 252
 SG+TG+ I+VDSG+
 Sbjct: 240 SGITGQIIYVDSGY 253

☐ >gi|22966064|gb|ZP_00013661.1| hypothetical protein [Rhodospirillum rubrum]
 Length = 339

Score = 213 bits (542), Expect = 2e-54
 Identities = 116/253 (45%), Positives = 158/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L K +++G+AN RSIA+G+AK GA + FTY L+ E HL
 Sbjct: 68 LAGKKGLVLGVANDRSIAWGIKAASDAGASIAFTYQGDPLLKRVKPLVEGLS--ERHLL 125

Query: 64 QIDVQSDEEVING-FEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122
 +DE ++ F + + G ID V H++AF++ + L+G + T+RE F IS
 Sbjct: 126 MPCDVTDEASLDAVFATLKETWGTIDFVVHAVAFAFSDKDQLKGHYMHTTRENFOQTMLISV 185

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 +S T +A A ++M +GG+++ TY G E + +YNVMGVAKA+LEA+V+YLA DLG
 Sbjct: 186 FSFTDIARRASEIMNDGGAMITLTYGAEVRMPHYNVMGVAKAALEASVRYLAADLGGRG 245

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSGVT 242
 IRVNAISAGPI+TL+A G+G F ILK E +PL+RNV EVG + YLLSDLS GVT
 Sbjct: 246 IRVNAISAGPIKTLAASGIGDFRYILKWNEYSPLRRNVTIDEVGNISGLYLLSDLSRGVT 305

Query: 243 GENIHVDSGFHAI 255
 GE HVDSG+H +
 Sbjct: 306 GEVHHVDSGYHLV 318

☐ >gi|23055279|gb|ZP_00081394.1| hypothetical protein [Geobacter metallireducens]
 Length = 256

Score = 210 bits (534), Expect = 2e-53
 Identities = 123/253 (48%), Positives = 163/253 (64%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L+ K VI GIAN++SIA+ +A+ + GA+L TY + + +

Sbjct: 4 LDGKKAVIFGIANEKSIAWAIAQAFFREGAELAVTYANETVAKRVIPLAESVGA--SLVL 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
DV++D E+ + FE+IGK G ID + HSIAFA E+L+G F T+REGF LA DIS+Y

Sbjct: 62 PCDVRNDAEIQSVFEEIGKAWGGIDILVHSIAFAGKEELKGSFLNTTREGFALALDISAY 121

Query: 124 SLTIVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
SL + A M GS++A TY GG+ NYNVMGVAKA+LE +VKYLA +G D

Sbjct: 122 SLIALMKAAHPFMAGREGSVLALTYGGQKVPNYNVMGVAKAALEMSVKYLAEAVGSDG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
IRVNAISAGP++TL++ GVGGFN I + E+APL+RN+ Q EV A YL S L+SGV+

Sbjct: 182 IRVNAISAGPLKTLASSGVGGFNQIAGHVAEKAPLRRNISQDEVAGAAVYLASSLASGVS 241

Query: 243 GENIHVDSGFHAI 255
GE VDSG++ I

Sbjct: 242 GEIHFVDSGYNII 254

☐ >gi|27377740|ref|NP_769269.1| NADH-enoyl acyl carrier protein reductase [Bradyr
japonicum]
gi|27350885|dbj|BAC47894.1| NADH-enoyl acyl carrier protein reductase [Bradyrhizo
japonicum]
Length = 271

Score = 210 bits (534), Expect = 2e-53
Identities = 119/252 (47%), Positives = 158/252 (62%), Gaps = 4/252 (1%)

Query: 4 LENKTYVIMGIANKRISIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
++ K V++G+AN RSIA+G+AK GA+L FTY ++ L

Sbjct: 8 MQGKRGVVLGVANNRSIAWGIKACHAAGAELAFTYQGDALKKRVEPLAAEIGG--LVLG 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
DV + F + + G ID + H+IA+ E L GR+ +T++E F + IS Y

Sbjct: 66 HCDVTDAATIDAAFAVLKEKWGKIDFLVHAIAYG--EQLDGRYVDTTQENFSKSMILISCY 123

Query: 124 SLTIVAHEAKKLMPGGSSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
S T VA A+KLM +GGS++ +Y G E + +YNVMGVAKA+LEA+V+YLA DLG NI

Sbjct: 124 SFTAVAQRAEKLMTDGGSLITLSYYGAEKWMPHYNVMGVAKAALEASVRYLAADLGEKNI 183

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
RVNAISAGPI+TL+A G+G F ILK E APL+RNV +VG +A Y LSDLS GVTG

Sbjct: 184 RVNAISAGPIKTLAASGIGDFRYILKWNEHNAPLRRNVSTEDVGGSALYFLSDLRSGVTG 243

Query: 244 ENIHVDSGFHAI 255
E HVDSG+H +

Sbjct: 244 EVHHVDSGYHVL 255

☐ >gi|23059616|ref|ZP_00084568.1| hypothetical protein [Pseudomonas fluorescens P
Length = 308

Score = 209 bits (532), Expect = 4e-53
Identities = 112/252 (44%), Positives = 155/252 (61%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRISIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L K +I+G+A+K SIA G+A + + GA+L FTY +

Sbjct: 48 LAGKRVLIVGVASKLSIASGIAAAMHREGAELAFETYQNDKLKGRVEEFAQGWGSSPELCF 107

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
 DV SDEE+ FE++ K +D + HS+ FA + L G F+E T+REGF +A DIS+

Sbjct: 108 PCDVASDEEIAKVFEELSKKWDGLDCIVHSVGFAPGDQLDGDFTTEATTREGFRIAHDISA 167

Query: 123 YSLTIVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPD 181
 YS +A +++M GS++ +YLG E + NYNVMG+AKASLEA V+YLA LGPD

Sbjct: 168 YSFVALAKAGREMMKGRNGSLTLTSLYGAERTMPNYNVMGMAKASLEAGVRYLAGSLGPD 227

Query: 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGV 241
 RVN +SAGPIRTL+A G+ F +L E + PL+RVN EVG A+L SDL+SG+

Sbjct: 228 GTRVNCVSAGPIRTLAASGIKNFRKMLAANEAQTPLRRNVTTIEEVGNAGAFCLSDLASGI 287

Query: 242 TGENIHVDSGFH 253
 +GE ++VD GF+

Sbjct: 288 SGEIMYVDGGFN 299

☐ >gi|23015709|gb|ZP_00055478.1| hypothetical protein [Magnetospirillum magnetotacticus]
 Length = 289

Score = 208 bits (529), Expect = 7e-53
 Identities = 115/258 (44%), Positives = 161/258 (62%), Gaps = 14/258 (5%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 + K ++MG+AN RSIA+G+A+ GA+L FTY +P A

Sbjct: 25 MAGKKGLVMGVANDRSIAWGIAQAARAQGAELAFETYQGEALEKRV-----RPLAQSV 76

Query: 64 QIDV-----QSDEEVING-FEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETTSREGFLLA 117
 D+ SDE I+ F ++ K G +D V H+I +++ +LRGR+++TS + FL +

Sbjct: 77 GSDIVLPCDVSDEASIDAVFAELEKRWGKLDFVVAIGYSDKNELRGRYADTSLQNFLTSL 136

Query: 118 QDISSYSLTIVAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALD 177
 IS +S T VA A +MP+GGS++ TY G E + +YNVMGV KA+LEA+V+YLA+D

Sbjct: 137 MHISVFSFTSVARRASAMMPDGGSLTLTYGAERVMPHYNVMGVCKAALEASVRYLAVD 196

Query: 178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDL 237
 LG IRVN++SAGPI+TL+A G+G F ILK E +PLKRVN ++G YLLS L

Sbjct: 197 LGGQGIRVNSLSAGPIKTLAASGIGDFRYILKWNEYSPLKRVNTLEDIGGAGLYLLSGL 256

Query: 238 SSGVTGENIHVDSGFHAI 255
 SSGV+GE HVD G+H +

Sbjct: 257 SSGVSGETHHVDCGYHV 274

☐ >gi|22970115|gb|ZP_00017264.1| hypothetical protein [Chloroflexus aurantiacus]
 Length = 282

Score = 207 bits (528), Expect = 8e-53
 Identities = 115/252 (45%), Positives = 157/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 +E K +I+G+AN RSIA+G+A+ L + GA + FTY LN P +

Sbjct: 26 MEGKKGLILGVANDRSIAWGIAQALHREGATIGFTYLGALERRVRPLAESLNSP--LIV 83

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETTSREGFLLAQDISSY 123

DV DE++ EQ + G ID + H+IAFAN E+L G T+REGF +A +IS+Y
 Sbjct: 84 PCDVSKDEITALIEQARETFGQIDFLVHAI AFANKEELSGTILNTTREGFRIALEISAY 143
 Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SL + A+ + S++ TY G + +YNVMGVAKA+LEA+V+YLA LGP I
 Sbjct: 144 SLIALVKAAEPIFAPDASVLTLYHGARQVIGSYNVMGVAKAALEASVRYLAAGLGPRGI 203
 Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNV DQVEVGKTAAYLLSDLSSGV TG 243
 RVNAISAGPIRTL+A G+ F ++ K E APL+RNV +VG A YL S L++GVTG
 Sbjct: 204 RVNAISAGPIRTLAASGIANFRSLHKKHFAEYAPLRRNV TIEDVGNAALYLCSP LAAGVTG 263
 Query: 244 ENIHVDSGFHAI 255
 E +VD+GF+ +
 Sbjct: 264 EIHVVDAGFN VV 275

>gi|23103009|gb|ZP_00089502.1| hypothetical protein [Azotobacter vinelandii]
 Length = 264

Score = 207 bits (527), Expect = 1e-52
 Identities = 113/252 (44%), Positives = 156/252 (61%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L K +I+G+A+K SIA G+A + + GA+L FTY +
 Sbjct: 4 LAGKRVLIVGVASKLSIASGIAAAMHREGAELAFETYQNDKLKGRVEEFAAGWGSSPELCF 63
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
 DV SDE++ FE++GK +D + HS+ FA + L G F+E TSR+GF +A DIS+
 Sbjct: 64 PCDVASDEDIARVFEELGKKWDGLDCIVHSVGFAPGDQLNGDFTVTSR DGFKIAHDISA 123
 Query: 123 YSLTIVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPD 181
 YS +A ++LM GS++ +YLG E + NYNVMG+AKASLEA V+YLA LGP+
 Sbjct: 124 YSFVALAKAGRELMKGRNGSLTSLYLGAE RTMPNYNVMGMAKASLEAGVRYLAASLGPE 183
 Query: 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNV DQVEVGKTAAYLLSDLSSGV 241
 RVN ISAGPIRTL+A G+ F +L E + PL+RNV EVG A+L SDL+SG+
 Sbjct: 184 GTRVNCISAGPIRTLAASGIAFRKMLAANERQTPLRRNV TIEEVGNAGAF LCSDLASGI 243
 Query: 242 TGENIHVDSGFH 253
 +GE ++VD GF+
 Sbjct: 244 SGEILYVDGGFN 255

>gi|15602047|ref|NP_245119.1| FabI [Pasteurella multocida]
 gi|12720402|gb|AAK02266.1| FabI [Pasteurella multocida]
 Length = 260

Score = 206 bits (523), Expect = 3e-52
 Identities = 112/253 (44%), Positives = 159/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L NK +I G+A+ RSIA+G+A+ + + GA+L FTY +L +
 Sbjct: 4 LTNRIL IAGVASNRSIAYGIAQAMKREGAELAFETYQNDKLKGRVEEFAKELGSDI--VI 61
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
 DV +DE + F ++ K DG HSIAFA + L G + + +REGF +A D+SS
 Sbjct: 62 PCDVGTDESIEQCFAELAKHWEKFDG FVHSIAFAPGDQLDGDYVD AVNREGFRIAH DVSS 121

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YS +A A+ ++ +++ +YLG E A+ NYNVMG+AKASLEAN +++A LG D
 Sbjct: 122 YSFVAMAKAARGMLNPNSALLTSLYGAERAIPNYNVMGLAKASLEANTRFMAAALGKDG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
 IRVNAISAGPIRTL+A G+ F +L E+ APL+R V +VG +AA+L SDLS+G+T
 Sbjct: 182 IRVNAISAGPIRTLAASGIKNFKMLANFEQTAPLRRTVTIEDVGNSAAFLCSDLSAGIT 241

Query: 243 GENIHVDSGFHAI 255
 GE +HVD+GF +
 Sbjct: 242 GEVVHVDAGFSIV 254

☐ >gi|13474637|ref|NP_106206.1| enoyl-[acyl-carrier-protein] reductase [Mesorhizobium loti]
 gi|14025391|dbj|BAB51992.1| enoyl-[acyl-carrier-protein] reductase [Mesorhizobium loti]
 Length = 267

Score = 204 bits (519), Expect = 9e-52
 Identities = 113/252 (44%), Positives = 156/252 (61%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 ++ K ++MG+AN SIA+G+AK L + GA+L FTY +L + +
 Sbjct: 5 MKGKRGLVMGVANDHSIAWGIKKLSEHGAELAFTYQGDAGFRRVKPLADKLGA--SLVV 62

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSRREGFLLAQDISSY 123
 DV+ V FE +GK+ G +D V H+I F++ +L+G +++TSR+ F+ IS Y
 Sbjct: 63 PCDVEDSASVAATFETLGKEWGGLDFVHHAIGFSDKNELKGLYADTSRDNFVRTMVISCY 122

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 S T VA A LM EGG++ TY G + NYNVMGVAKA LEA+V+YLA D GP I
 Sbjct: 123 SFTEVARNAALMTEGGSMITLTYAGSVRVMPNYNVMGVAKAGLEASVRYLANDYGPRGI 182

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVN ISAGP+RTL+ G+ + + +PL+R V EVG +A YLLSDL+SGVTG
 Sbjct: 183 RVNGISAGPVRTLGAAGISDARHMFSYQQRNSPLRRTVTIDEVGGSSALYLLSDLASGVTG 242

Query: 244 ENIHVDSGFHAI 255
 E +VDSG+H +
 Sbjct: 243 EIHVDSGYHIV 254

☐ >gi|17988241|ref|NP_540875.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella melitensis]
 gi|23503018|ref|NP_699145.1| enoyl-(acyl-carrier-protein) reductase [Brucella melitensis]
 gi|25283462|pir||AH3496 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.1)
 [imported] - Brucella melitensis (strain 16M)
 gi|17984008|gb|AAL53139.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella melitensis]
 16M]
 gi|23349059|gb|AAN31060.1|AE014503.7 enoyl-(acyl-carrier-protein) reductase [Brucella melitensis]
 Length = 272

Score = 204 bits (519), Expect = 1e-51
 Identities = 118/253 (46%), Positives = 158/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 ++ K +IMG+AN S+A+G+AK L GA+L FTY Q+ +
 Sbjct: 5 MQGKRGLIMGVANNHSLAWGIAKQLAAQGAELAFTYQGDALGKRVKPLAEQVGSD--FVL 62

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
 DV+ V FE+I K G +D + H+I F++ +L+GR+++ T+RE F IS+
 Sbjct: 63 PCDVEDIATVDAVFEEIEKKWGGLDFLVHAIGFSDKTELKGRYADVTTRENFSTRMVIS 122

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YS T VA A+KLM +GGS+ TY G + NYNVMGVAKA+LEA V+YLA D GP
 Sbjct: 123 YSFTEVAQRAEKLMDGGSILTLTYGGSTRIPNYNVMGVAKAALEAMVRYLAADYGPQG 182

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
 IRVNAISAGP+RTL+ G+G I +PL+R VD +VGK+A YLLSDLSSGVT
 Sbjct: 183 IRVNAISAGPVRTLGAAGIGDARAIFSYQRRNSPLRRTVDIDDVGKSAVYLLSDLSSGVT 242

Query: 243 GENIHVDSGFHAI 255
 GE VDSG++ +
 Sbjct: 243 GEIHVDSGYNIV 255

☐ >gi|15792718|ref|NP_282541.1| putative enoyl-[acyl-carrier-protein] reductase [1
 [Campylobacter jejuni]
 gi|11250877|pir|H81284 probable enoyl-[acyl-carrier-protein] reductase (NADH2) (
 1.3.1.9) Cj1400c [imported] - Campylobacter jejuni
 (strain NCTC 11168)
 gi|6968829|emb|CAB73824.1| putative enoyl-[acyl-carrier-protein] reductase [NADH]
 [Campylobacter jejuni subsp. jejuni NCTC 11168]
 Length = 274

Score = 203 bits (517), Expect = 2e-51

Identities = 116/250 (46%), Positives = 163/250 (65%), Gaps = 2/250 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHL 63
 ++ K +I+G+AN +SIA+G+AK GA+L FT+ + N +Y
 Sbjct: 3 MKGKKGLIVGVANNKSIAYGIAKACFDQGAELAFITLNDALKKRVEPIAQEFNS--NFVY 60

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
 ++DV ++E + + E+I KD+G ID V H++AFA E L F ETS+E F +A S Y
 Sbjct: 61 ELDVNNEHLDSIAEKIKKDLGEIDFVVHAVAFAPKEALENSFLETSKEAFDIAMQTSVY 120

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SL + ++ + GSI+ +YLG G V +YNVMGVAKA+LE++V+YLA DLG I
 Sbjct: 121 SLLSLTRAVLPILKDKGSILTSLYLGGVKYVPHYNVMGVAKAALESSVRYLARDLGVKGI 180

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVNAISAGPI+TL+A G+G F ILK E +PLKRN +VG +A YLLSDL++GVTG
 Sbjct: 181 RVNAISAGPIKTLAASGIGDFRMILKYNEINSPLKRNVSIEDVGNSAMYLLSDLANGVTG 240

Query: 244 ENIHVDSGFH 253
 E +VD+G++
 Sbjct: 241 EIHVVDAGYN 250

☐ >gi|15611251|ref|NP_222902.1| ENOYL-ACYL CARRIER PROTEIN REDUCTASE [Helicobacter
 gi|6685452|sp|Q9ZMN7|FABI_HELPJ Enoyl-[acyl-carrier-protein] reductase [NADH] (NA
 enoyl-ACP reductase)
 gi|7431095|pir||B71964 enoyl-acyl carrier protein reductase - Helicobacter pylori
 J99)
 gi|4154700|gb|AAD05765.1| ENOYL-ACYL CARRIER PROTEIN REDUCTASE [Helicobacter pylo

Length = 275

Score = 203 bits (516), Expect = 2e-51

Identities = 112/252 (44%), Positives = 160/252 (63%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSI AFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L+ K +I+G+AN +SIA+G+A+ GA L FTY +LN P ++Y

Sbjct: 4 LKGKGLIVGVANNKSIAYGIAQSCFNQGATLAFTYLNESLEKRVRP I AQELNSP--YVY 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
 ++DV +E + + I +D+G++D + HS+AFA E L G ETS+ F A +IS Y

Sbjct: 62 ELDVSKEEHFKSLYNNIKQDLGSLDFIVHSVAFAPKEALEGSLLETSSKSAFNTAMEISVY 121

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
 SL + + K L+ G S++ +YLG + +YNVMG+AKA+LE+ V+YLA+DLG NI

Sbjct: 122 SLIELTNTLTKPLLNNGASVLTLSYLGSTKYMAYHNVNMG LAKAALES AVRYLAVDLGKHNI 181

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
 RVNA+SAGPIRTL++ G+ F ILK E APL++NV EVG YLLS LS+GV+G

Sbjct: 182 RVNALSAGPIRTLASSGIADFRMILKWNEINAPLRKNVSLEEVGNAGMYLLSSLSNGVSG 241

Query: 244 ENIHVDSGFHAI 255
 E VD+G+H +

Sbjct: 242 EVHFVDAGYHVM 253

☐ >gi|17545891|ref|NP_519293.1| PROBABLE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]
 OXIDOREDUCTASE [Ralstonia solanacearum]
 gi|17428186|emb|CAD14874.1| PROBABLE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]
 OXIDOREDUCTASE [Ralstonia solanacearum]
 Length = 264

Score = 203 bits (516), Expect = 2e-51

Identities = 115/251 (45%), Positives = 153/251 (60%), Gaps = 3/251 (1%)

Query: 4 LENKTYVIMGIANKRSI AFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L K +I G+ + RSIA+G+A + GA+L FTY + ++

Sbjct: 4 LAGKRILITGLLSNRSIAYG IASACKREGAELAFYVGERFKDRIT E FAN EFGS--QLVF 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
 DV SDE++ F +G+ + DG+ HSI FA E + G F + SRE F +A DIS+

Sbjct: 62 DCDVGSDEQIAKVFADLGQHWDFDGLVHSIGFAPREAIAGDFLDGLSREAFRIAHDISA 121

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YS +A A ++ S++A TYLG E V NYN MGVAKA+LEA V+YLA LGP

Sbjct: 122 YSFPALAKAALPMLSPNASLLALTYLGAERVVPNYNTMGVAKAALEACVRYLASALGPKG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
 IR N ISAGPI+TL+A G+ F +LK +E+ APL+RNV EVG AA+LLSDLSSG+T

Sbjct: 182 IRANGISAGPIKTLAASGIKDFGKLLKYMEDVAPLRNV TIEEVGNVAAFLSDLSSGMT 241

Query: 243 GENIHVDSGFHH 253
 GE +VD GF+

Sbjct: 242 GEITYVDCGFN 252

☐ >gi|26247623|ref|NP_753663.1| Enoyl-[acyl-carrier-protein] reductase [NADH] [Esc

CFT073]
gi|26108025|gb|AA080225.1|AE016760_84 Enoyl-[acyl-carrier-protein] reductase [NAD
CFT073]
Length = 262

Score = 202 bits (514), Expect = 4e-51
Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +
Sbjct: 4 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFITYQNDKLKGRVEEFQAQLGSDI--VL 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS
Sbjct: 62 QCDVAEDTSIDTMFAELGKVWPKFDGFGVHSIGFAPGDQLDGDYVNAVTRREGFKIAHDISS 121

Query: 123 YSLTIVAHEAKKLMPEGGSI VATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
YS +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+
Sbjct: 122 YSFVAMAKACRSM LNPGSALLTSLYLAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++
Sbjct: 182 VRVNAISAGPIRTLAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGIS 241

Query: 243 GENIHVDSGF 252
GE +HVD GF
Sbjct: 242 GEVVHVDGGF 251

gi|15801888|ref|NP_287908.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Esche
0157:H7 EDL933]
gi|15831115|ref|NP_309888.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Esche
0157:H7]
gi|16129249|ref|NP_415804.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Esche
K12]
gi|24112687|ref|NP_707197.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Shige
str. 301]
gi|119391|sp|P29132|FABI_ECOLI Enoyl-[acyl-carrier-protein] reductase [NADH] (NAD
enoyl-ACP reductase)
gi|1073371|pir||S48029 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9
Escherichia coli (strain K-12)
gi|25283445|pir||E90861 enoyl-[acyl-carrier-protein] reductase (NADH) ECs1861 [im
Escherichia coli (strain 0157:H7, substrain RIMD
0509952)
gi|25283451|pir||H85757 enoyl-[acyl-carrier-protein] reductase (NADH) [imported]
Escherichia coli (strain 0157:H7, substrain EDL933)
gi|9955169|pdb|1C14|A **S** Chain A, Crystal Structure Of E Coli Enoyl Reductase-Nad+
Complex
gi|9955170|pdb|1C14|B **S** Chain B, Crystal Structure Of E Coli Enoyl Reductase-Nad+
Complex
gi|20150083|pdb|1I2Z|A **S** Chain A, E. Coli Enoyl Reductase In Complex With Nad And
gi|20150084|pdb|1I2Z|B **S** Chain B, E. Coli Enoyl Reductase In Complex With Nad And
gi|20150085|pdb|1I30|A **S** Chain A, E. Coli Enoyl Reductase +nad+sb385826
gi|20150086|pdb|1I30|B **S** Chain B, E. Coli Enoyl Reductase +nad+sb385826
gi|23200396|pdb|1LX6|A **S** Chain A, Crystal Structure Of E. Coli Enoyl Reductase-Na
Bound Benzamide Inhibitor

gi|23200397|pdb|1LX6|B **S** Chain B, Crystal Structure Of E. Coli Enoyl Reductase-Na Bound Benzamide Inhibitor

gi|23200398|pdb|1LXC|A **S** Chain A, Crystal Structure Of E. Coli Enoyl Reductase-Na Bound Acrylamide Inhibitor

gi|23200399|pdb|1LXC|B **S** Chain B, Crystal Structure Of E. Coli Enoyl Reductase-Na Bound Acrylamide Inhibitor

gi|145851|gb|AAA17755.1| envM

gi|587106|emb|CAA55381.1| enoyl-ACP reductase [Escherichia coli]

gi|1787545|gb|AAC74370.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli]

gi|12515500|gb|AAG56524.1|AE005378_3 enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli]

gi|13361326|dbj|BAB35284.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli]

gi|24051603|gb|AAN42904.1|AE015155_11 enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli]

str. 301]

Length = 262

Score = 202 bits (513), Expect = 5e-51

Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRISIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +

Sbjct: 4 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFETYQNDKLGKRVEEFAAQLGSDI--VL 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS

Sbjct: 62 QCDVAEDASIDTMFAELGKVWPKFDGFGVHSIGFAPGDQLDGDYVNAVTVREGFKIAHDISS 121

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
YS +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+

Sbjct: 122 YSFVAMAKACRSMLNPGSALLTSLYGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++

Sbjct: 182 VRVNAISAGPIRTLAASGIKDFRKMALAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGIS 241

Query: 243 GENIHVDSGF 252
GE +HVD GF

Sbjct: 242 GEVHVVDGGF 251

>gi|2914323|pdb|1DFG|A **S** Chain A, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Benzo-Diazaborine

gi|2914324|pdb|1DFG|B **S** Chain B, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Benzo-Diazaborine


gi|2914325|pdb|1DFH|A **S** Chain A, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Thieno-Diazaborine


gi|2914326|pdb|1DFH|B **S** Chain B, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Thieno-Diazaborine


gi|2914327|pdb|1DFI|A **S** Chain A, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad


gi|2914328|pdb|1DFI|B **S** Chain B, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad


gi|2914329|pdb|1DFI|C **S** Chain C, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad


gi|2914330|pdb|1DFI|D  Chain D, X-Ray Structure Of Escherichia Coli Enoyl Reductase Bound Nad


gi|6137454|pdb|1QG6|A  Chain A, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan

gi|6137455|pdb|1QG6|B  Chain B, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan

gi|6137456|pdb|1QG6|C  Chain C, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan

gi|6137457|pdb|1QG6|D  Chain D, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan

gi|6435557|pdb|1D8A|A  Chain A, E. Coli Enoyl ReductaseNAD+TRICLOSAN COMPLEX

gi|6435558|pdb|1D8A|B  Chain B, E. Coli Enoyl ReductaseNAD+TRICLOSAN COMPLEX

gi|1742101|dbj|BAA14841.1| Enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3. dependent enoyl-ACP reductase). [Escherichia coli]

gi|1742110|dbj|BAA14849.1| Enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3. dependent enoyl-ACP reductase). [Escherichia coli]

Length = 261

Score = 202 bits (513), Expect = 5e-51

Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +

Sbjct: 3 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDI--VL 60

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS

Sbjct: 61 QCDVAEDASIDTMFAELGKVWPKFDGFGVHSIGFAPGDQLDGDYVNAVTRREGFKIAHDISS 120

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
YS +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+



Sbjct: 121 YSFVAMAKACRSMLNPGSALLTSLYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 180


Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++


Sbjct: 181 VRVNAISAGPIRTLAASGIKDFRKMALAHCEAVTPIRRTVTIEDVGNSAAFLCSDLGAGIS 240


Query: 243 GENIHVDSGF 252
GE +HVD GF


Sbjct: 241 GEVVHVDGGF 250


 >gi|5822339|pdb|1QSG|A  Chain A, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822340|pdb|1QSG|B  Chain B, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822341|pdb|1QSG|C  Chain C, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822342|pdb|1QSG|D  Chain D, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822343|pdb|1QSG|E  Chain E, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822344|pdb|1QSG|F  Chain F, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822345|pdb|1QSG|G [S] Chain G, Crystal Structure Of Enoyl Reductase Inhibition
Triclosan
gi|5822346|pdb|1QSG|H [S] Chain H, Crystal Structure Of Enoyl Reductase Inhibition
Triclosan
Length = 265

Score = 202 bits (513), Expect = 5e-51
Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +
Sbjct: 7 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFETYQNDKLGKRVEEFAAQLGSDI--VL 64

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS
Sbjct: 65 QCDVAEDASIDTMFAELGKVWPKFDGFGVHSIGFAPGDQLDGDYVNAVTVREGFKIAHDISS 124

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
YS +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+
Sbjct: 125 YSFVAMAKACRSMLNPGSALLTSLYGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 184

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++
Sbjct: 185 VRVNAISAGPIRTLAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGIS 244

Query: 243 GENIHVDSGF 252
GE +HVD GF
Sbjct: 245 GEVVHVDGGF 254

[>gi|15672548|ref|NP_266722.1| NADH-dependent enoyl-ACP reductase [Lactococcus la
lactis]
gi|25283448|pir|F86695 NADH-dependent enoyl-ACP reductase fabI [imported] - Lact
lactis subsp. lactis (strain IL1403)
gi|12723453|gb|AAK04664.1|AE006290_9 NADH-dependent enoyl-ACP reductase [Lactococ
lactis]
Length = 250

Score = 201 bits (512), Expect = 7e-51
Identities = 113/250 (45%), Positives = 158/250 (63%), Gaps = 4/250 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
LE K VIMG+AN +SIA+G AK + GA L++TY +L +PE L
Sbjct: 3 LEGKKIVIMGVANNKSIWGCAMKDKQATLIYTY---QNERMEKQLAKLAEPEDLLI 58

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 123
+ DV SDE + F I VG IDG+ H+IA++ E+L G ++ SR+G+ LAQDIS+Y
Sbjct: 59 ECDVTSDESIRRAFGTIEARVGKIDGLVHAIAYSKEELGGNVTDISR DG YALA QDISAY 118

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
SL VA AK L+ +G IV TY+G A+ NYNVMG+AKA+LE+ V+YLA ++ +
Sbjct: 119 SLLAVAKAAKPLLLKKGSGIVTLTYMGSVRAIPNYNVMGIAKAALESTVRYLAAEMAHVGV 178

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
VN ISAG I+TL+ GV G+ ++KE + R V +VG+TAA+L+S L+SGV G
Sbjct: 179 HVNGISAGAIKTLAVSGVSGYKDLIKESDSRTADGVGVTTIDVGTAAFLVSPASGVIG 238

Query: 244 ENIHVDSGFH 253

+ ++VD G H
Sbjct: 239 DIVYVDKGVH 248

>gi|27375882|ref|NP_767411.1| NADH-enoyl acyl carrier protein reductase [Bradyr
japonicum]
gi|27349020|dbj|BAC46036.1| NADH-enoyl acyl carrier protein reductase [Bradyrhizo
japonicum]
Length = 265

Score = 201 bits (512), Expect = 7e-51
Identities = 114/252 (45%), Positives = 158/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
++ K +IMGIAN SIA+G+AK L GA+L FT+ QL +
Sbjct: 5 MKGKRGILMGIANDHSIAWGMAKTLHAHGAELAFTFQGEALGKRVKPLAEQLGV--ELVL 62

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123
DV+ V F+ + + G +D V H+I FA+ +L+GR+++TSRE F IS +
Sbjct: 63 PCDVEDIASVDATFDVLRKWKGLDFVIHAIGFADKNELKGRYADTSRENFSRTMVISCF 122

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183
S T VA A +LM EGGS++ T+ E A+ NYNVMGVAKA+LEA+V+YLA D GP I
Sbjct: 123 SFTEVAKRAAELMTEGGSMTITLTFGASERAMPNYNVMGVAKAALEASVRYLASDFGPRGI 182

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243
RVNA+SAGPIRTL+ G+G + +++ +PL+R V E+G +A YLLSDLS GVTG
Sbjct: 183 RVNAVSAGPIRTLAGSGIGEARAMFAFMQKHSPLRRGVTLDELGGSALYLLSDLSSGVTG 242

Query: 244 ENIHVDSGFHAI 255
E +VDSG++ +
Sbjct: 243 EIHVDSGYNIV 254

>gi|22975990|gb|ZP_00021907.1| hypothetical protein [Ralstonia metallidurans]
Length = 260

Score = 201 bits (512), Expect = 7e-51
Identities = 113/253 (44%), Positives = 156/253 (61%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
L K +I G+ + RSIA+G+A + GA+L FTY + +Y
Sbjct: 4 LAGKRILITGLLSNRSIAYGIAAACKREGAELAFTYVGERFKDRITDFAKEFGSD--MIY 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
+ DV SDE++ F +G+ DG+ HSI FA E + G F + SREGF +A DIS+
Sbjct: 62 ECDVGSDEQIDATFAALGQRWEKFDGLVHSIGFAPREAIAGNFDGLSREGFRIAHDISA 121

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
YS +A A L+ + S++ TYLG E V NYN MG+AKASLEA+V+YLA +GP
Sbjct: 122 YSFPALAKAAMPLNLDKASLLTLTYLGAERVVPNYNTMGLAKASLEASVRYLASAVGPRG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
+R N ISAGPI+TL+A G+ F+ +LK E+ AP++RNV EVG AA+LLSDL+SGVT
Sbjct: 182 MRANGISAGPIKTLAASGIKDFSRLKHFEDVAPIRRNVITIEEVGNVAAFLSDLASGVT 241

Query: 243 GENIHVDSGFHAI 255

GE +VD G++ +
 Sbjct: 242 GEITYVDGGYNIV 254

☐ >gi|22982236|ref|ZP_00027522.1| hypothetical protein [Burkholderia fungorum]
 Length = 274

Score = 201 bits (512), Expect = 7e-51
 Identities = 110/253 (43%), Positives = 158/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSLAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXXXXXXQLNQPEAHLY 63
 L K ++ G+ + RSIA+G+A+ + GA+L FTY + ++
 Sbjct: 15 LAGKRILLTGLLSNRSIAYGIAQACRREGAELAFITYVGERFKDRIKEFAGEFGSD--LVF 72

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122
 DV D ++ F + + +DG+ HSI FA E + G F + +RE F +A DIS+
 Sbjct: 73 PCDVADDAQIDALFASLKQHWGDLGLVHSIGFAPREAIAGDFLDGMTRENFRIAHDISA 132

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
 YS +A A+ + S++ +YLG E A+ NYN MG+AKASLEA+V+YLA+ LG
 Sbjct: 133 YSFPALAKAAQSMFTPDASLLTLSYLGAEARIPNYNTMGLAKASLEASVRYLAVSLGAKG 192

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242
 +RVN ISAGPIRTL+A G+ GF IL+ +E+ APL+RVN +VG TAA+LLSDL++GVT
 Sbjct: 193 VRVNGISAGPIRTLAASGIKGFGLKILEFVEQNAPLRNVITIEQVGNTAAFLLSDLAAGVT 252

Query: 243 GENIHVDSGFHAI 255
 E +HVDSGF+A+
 Sbjct: 253 AEIVHVDSGFNAV 265

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Mar 26, 2003 11:48 PM
 Number of letters in database: 445,599,717
 Number of sequences in database: 1,384,147

Lambda K H
 0.316 0.135 0.368

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 190,169,730
 Number of Sequences: 1384147
 Number of extensions: 7112778
 Number of successful extensions: 21006
 Number of sequences better than 10.0: 1996

Number of HSP's better than 10.0 without gapping: 777
Number of HSP's successfully gapped in prelim test: 1219
Number of HSP's that attempted gapping in prelim test: 19003
Number of HSP's gapped (non-prelim): 2046
length of query: 256
length of database: 445,599,717
effective HSP length: 121
effective length of query: 135
effective length of database: 278,117,930
effective search space: 37545920550
effective search space used: 37545920550
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.6 bits)
S2: 71 (32.0 bits)